

HETEROSIS AND INHERITANCE PATTERN OF YIELD TRAITS IN BREAD WHEAT (*Triticum aestivum* L.)

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Wheat (*Triticum aestivum* L.) occupies a prominent position in cropping pattern of Pakistan since it is the main staple food for rapidly increasing population of the country. Keeping in view the importance of wheat production, the prime objective of the study was to investigate the genetics and heredity control of the yield related traits. To achieve the objective a 4×4 diallel cross was attempted using Punjab-11, RARI-6026, Uqab-2000 and Renya-23 genotypes. The F₁ was evaluated using RCBD with three replications in the experimental area of Plant Breeding and Genetics, UCA&ES, The Islamia University of Bahawalpur. The data were taken for yield related traits i.e. days to heading, flag leaf area (cm²), number of tillers/plant, plant height (cm), spike length (cm), number of spikelets/spike, number of grains/spike, grain weight/spike (g), seed index (g) and grain yield/plant (g). The analysis of variance depicted significant differences among the genotypes for all the studied traits. The cross Renya-23 × Punjab-11 exhibited maximum possible degree of heterobeltiosis for days to heading (-12.2), flag leaf area (5.3), tillers per plant (10.7), plant height (-8.2), grain weight per spike (18.5) and grain yield per plant (18.4) which may be used in further breeding programs for selecting transgressive segregates in the segregating generations. The genetic analysis revealed that additive gene action with partial dominance was controlling the heredity of all the traits studied. Presence of heterobeltiosis along with additive gene action suggests the potential of above mentioned genotypes for developing new high yielding wheat cultivars.

Keywords: Genetic diversity, heterobeltiosis; yield related traits, heredity control

INTRODUCTION

Wheat (*Triticum aestivum* L.) is staple food in near half of the world. Wheat is one of the most important crops of the Pakistan. It contributes 14.4 % to the value added in agriculture it has 3 percent share in national GDP. From last decade, there is no significant improvement in the yield of wheat and even varieties are not performing in the field very well (Rashid *et al.* 2013). Main reason of the lower average production is marginal lands and low availability of farm inputs. To cope with this problem, it is essential to develop such genotypes which can perform well on marginal lands and even with low inputs. So, development and evaluation of new germplasm is need of the time.

Genetic advancement in wheat take place by natural selection and other methods adopted by human since the primitive times of wheat domestication. Knowledge of inheritance of parental genotypes and genetic mechanism controlling grain production and other related parameters is much essential to organize an appropriate breeding strategy. Genetic studies estimate that whether selection would be fruitful in early segregating population for the betterment of a particular character or in advanced generation. The presence of genes which act additively to control a

parameter suggests that making selection in early generation may be advantageous to improve a character while dominance or over dominance favours selection for advanced generations for the parameters under consideration (Adel and Ali, 2013). Therefore, a sufficient information regarding the inheritance pattern and mode of gene action controlling the expression of a parameter under selection is of great significance (Munis *et al.* 2012).

Studies of the heterosis and heterobeltiosis provide valuable data that can be used in making combinations of parents for hybridization and can be useful in breeding programs (Bilgin *et al.* 2011). Knowledge of heredity control and genetics of yield and yield related traits is crucial to establish an appropriate breeding program to develop new genotypes.

Keeping in view the constraints in the production and future needs the aim of the study was to evaluate the genotypes to be used in the development of new germplasm and to investigate the heredity control and genetics of different yield related traits in bread wheat.

MATERIALS AND METHODS

The present study was carried out at research farm of Department of Plant Breeding and Genetics, UCA & ES,

The Islamia University Bahawalpur (situated at 29.4° North latitude, 71.68° East longitude and 116 meters above sea level).

Heterosis and genetic analysis After genetic diversity studies, four genotypes namely Punjab-11, RARI-6026, Uqab-2000 and Renya-23, sown on November 25, 2014. At heading, the parental genotypes were intermated using full diallel mating system (4×4) to generate 12 F_1 hybrids (direct and indirect). Seed of F_1 crosses along with the parents were sown in randomized complete block design with three replications on November 27, 2015. Each replication consisted of 10 meter long six rows of each genotype including parents and F_1 hybrids with a plant to plant distance of 20cm and row to row distance of 30 cm. Seeds were sown at field capacity moisture level and after planting of experimental material, four irrigations (each of 75mm) were applied during active growing period (each a germination, tillering, booting and grain formation). Other agronomic practices weeding and fertilization application (NPK @ 100-40-0 Kg ha⁻¹) were applied equally to all genotypes. At maturity, data were recorded for days to 50% heading, number of tillers per plant, plant height, Spike

length, number of spikelet per spike, number of grains per spike, grain yield per spike, seed index, grain yield per plant (g) and flag leaf area. Flag leaf area was measured by using the formula given by Muller (1991). Data for each trait were collected from 10 plants and average was calculated for statistical analysis.

All collected data were subjected to analysis of variance (Steel et al. 1997). Better parent heterosis (heterobeltiosis) was calculated according to Fonseca and Patterson (1968). Genetic control of yield and yield related traits was determined by performing genetic analysis using the method given by Hayman (1954) and Jinks (1954).

RESULTS

Genetic Analysis and Heterosis: Variance analysis depicted highly significant genotypic differences for all the traits under study (Table 1). Estimates of better parent heterosis (heterobeltiosis) are presented in Table 2. Joint regression analysis (Table 3) proved that data is fit for additive-dominance model for all the characters under study. Trait by trait results and discussion are described below.

Table 1: Genotypic mean squares of different agronomic traits as obtained from a 4x4 diallel crosses of wheat.

Source of variance	Degree of freedom (n-1)	Mean squares
Days to heading	15	29.2**
Flag leaf area	15	84.2**
No. of tillers/plant	15	9.1**
Plant height	15	14.6**
Spike length	15	2.3**
No. of spikelets/spike	15	3.3*
No. of grains/spike	15	11.3**
Grain weight/spike	15	0.36**
Seed index	15	3.8**
Grain yield/plant	15	16.9**

* - significant at 0.05% probability level

** - significant at 0.01 % probability level

For days to heading the genotype Renya-23 \times Punjab-11 exhibited maximum possible degree of better parent heterosis i.e. - 12.2 % (Table 2) and from Wr/Vr Graph (Figure 1. a) it is evident that Punjab-11 possessed maximum number of dominant genes due to its location on the graph. In case of flag leaf area maximum heterosis (5.3%) was found for hybrid Renya-23 \times Punjab-11 but this value is too small to be used in breeding program. For this trait the genotype Renya-23 possessed maximum dominant genes as being closest to the origin on Wr/Vr graph (Figure 1. b). The hybrid Renya-23 \times Punjab-11 showed maximum significant positive heterobeltiosis (10.7 %) for number of tillers per plant (Table 2) and distribution of array point along the regression line, the genotype RARI-6026 seemed to possess maximum dominant genes as it occupied a position nearest to the origin (Figure 1. c). Ross Renya-23 \times Punjab-11 showed maximum heterobeltiosis (- 8.2) for plant height but in a negative direction (Table 2). Distribution of parental genotypes along the regression line showed that RARI-6026 had maximum dominant genes as it is nearest to

the origin (Figure 1. d) for plant height. The hybrid Renya-23 \times Punjab-11 showed maximum and significantly positive superior parent heterosis (9.3%) for spike length whereas Arrangement of array points along the regression line showed that Punjab 11 possessed maximum dominant genes (Figure 1. e) for this trait. The hybrid Renya-23 \times Punjab-11 displayed the maximum degree of better parent heterosis (8.0 %) for spikelets per spike and seed index (8.9%). It was evident from Wr/Vr Graph (Figure 1. f, h) that genotype Punjab-11 contained maximum number of dominant genes for spikelets per spike and Renya-23 contains maximum dominant genes for seed index because of it's array point position on the origin. The hybrids Renya-23 \times Punjab-11 exhibited maximum and significant increased hybrid vigour over better parent i.e. 8.7 % for number of grains per spike, grain weight per spike i.e. 18.5% and grain yield per plant i.e. 18.4 % (Table 2) whereas the genotype RARI-6026 appeared nearest to the origin indicating to have maximum dominant genes for number of grains per spike and grain weight per spike (Figure 1. g, i) and genotypes Renya-23

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contained maximum dominant genes for grain yield per plant (Figure 1, j).

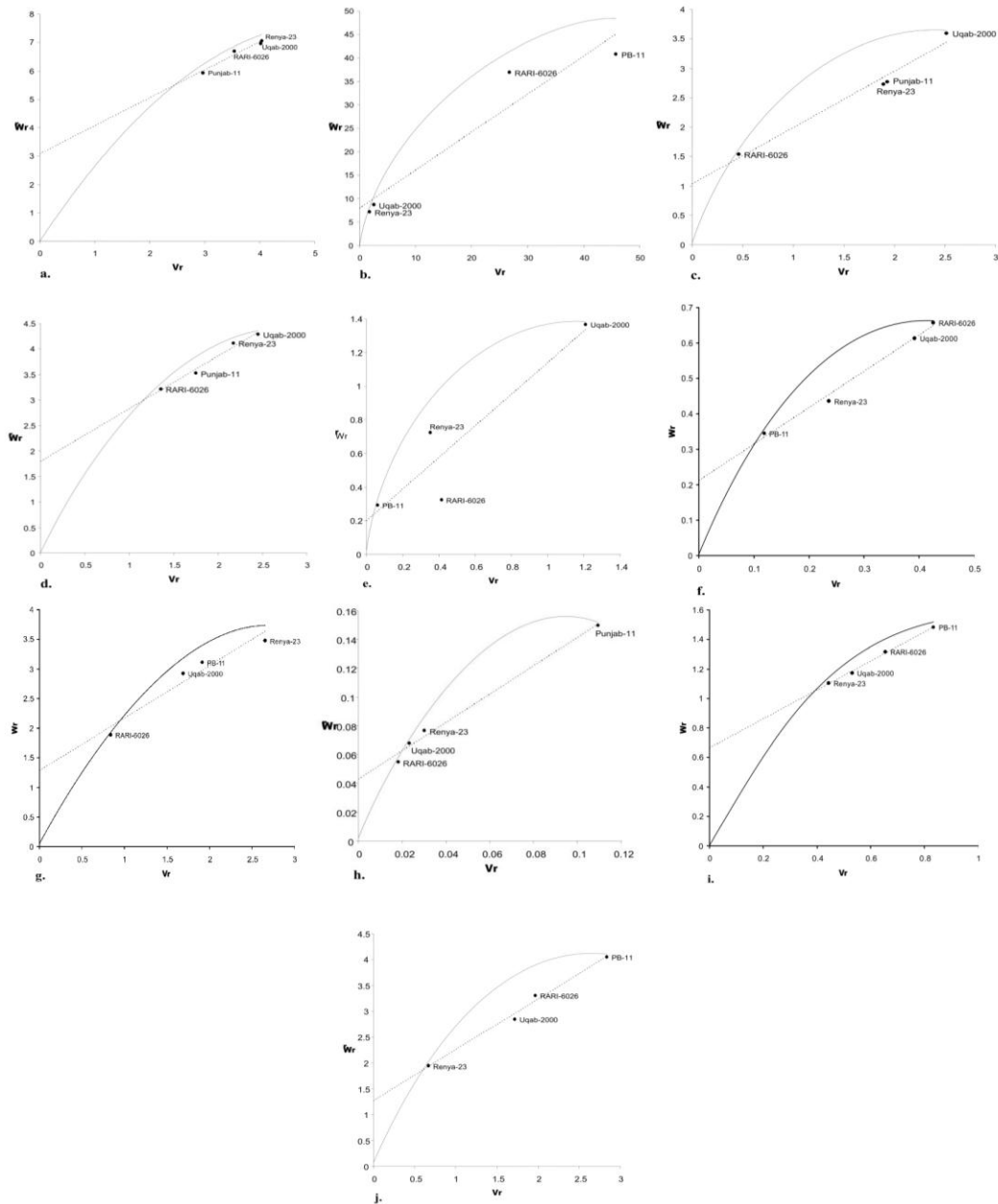


Figure 1 : Wr/Vr graph for a) days to heading b) flag leaf area c) number of tillers per plant d) plant height e) spike length f) number of spikelets per spike g) number of grains per spike h) grain weight per spike i) seed index and j) grain yield per plant

Table 2: Magnitude of better parent heterosis (heterobeltiosis) for different agronomic traits as obtained from 4×4 diallel cross.

crosses	Days to heading	Flag leaf area	Tillers/ plant	Plant height	Spike length	Spikelets/ spike	Grains/ spike	Grain weight/spike	Seed index	Grain yield/plan t
Punjab-11 × RARI-6026	- 0.3 ^{NS}	- 1.8 ^{NS}	2.3 [*]	0.0	3.8 ^{**}	0.4 ^{NS}	- 2 ^{NS}	2.8 [*]	0.0	0.1 ^{NS}
Punjab-11 × Uqab-2000	0.4 ^{NS}	- 1.8 ^{NS}	1.3 ^{NS}	- 1.5 ^{NS}	0.0	1.2 ^{NS}	0.0	- 1.9 ^{NS}	2.3 [*]	2.7 [*]
Punjab-11 × Renya-23	- 0.6 ^{NS}	0.0	0.6 ^{NS}	- 0.3 ^{NS}	- 1.1 ^{NS}	0.0	1.2 ^{NS}	0.0	2.3 [*]	- 1.03 ^{NS}
RARI-6026 × Punjab-11	- 0.3 ^{NS}	0.0	2.0 ^{NS}	0.0	1.2 ^{NS}	- 2.2 ^{NS}	- 1.7 ^{NS}	2.5 [*]	- 2.1 ^{NS}	- 1.9 ^{NS}
RARI-6026 × Uqab-2000	0.0	- 1.9 ^{NS}	- 1.1 ^{NS}	0.0	- 1.2 ^{NS}	- 0.4 ^{NS}	3.5 ^{**}	- 1.5 ^{NS}	- 1.1 ^{NS}	0.0
RARI-6026 × Renya-23	1.6 ^{NS}	- 1.0 ^{NS}	- 2.2 ^{NS}	1.5 ^{NS}	0.0	- 1.7 ^{NS}	0.0	- 1.5 ^{NS}	2.0 ^{NS}	- 0.2 ^{NS}
Uqab-2000 × Punjab-11	- 7.8 ^{**}	4.3 ^{**}	4.1 ^{**}	- 8.0 ^{**}	8.9 ^{**}	4.6 ^{**}	8.6 ^{**}	8.6 ^{**}	6.1 ^{**}	14.9 ^{**}
Uqab-2000 × RARI-6026	0.0	- 2.1 ^{NS}	2.3 [*]	- 0.3 ^{NS}	- 2.0 ^{NS}	4.7 ^{**}	- 1.2 ^{NS}	- 1.5 ^{NS}	0.0	2.7 [*]
Uqab-2000 × Renya-23	1.0 ^{NS}	0.0	1.1 ^{NS}	- 0.7 ^{NS}	2.0 ^{NS}	- 0.4 ^{NS}	1.7 ^{NS}	1.6 ^{NS}	2.0 ^{NS}	1.3 ^{NS}
Renya-23 × Punjab-11	- 12.2 ^{**}	5.3 ^{**}	10.7 ^{**}	- 8.2 ^{**}	9.3 ^{**}	8.0 ^{**}	8.7 ^{**}	18.5 ^{**}	8.9 ^{**}	18.4 ^{**}
Renya-23 × RARI-6026	1.6 ^{NS}	0.9 ^{NS}	- 2.2 ^{NS}	0.3 ^{NS}	0.0	0.0	- 1.2 ^{NS}	- 1.5 ^{NS}	- 0.2 ^{NS}	0.0
Renya-23 × Uqab-2000	- 5.1 ^{**}	- 2.1 ^{NS}	1.1 ^{NS}	- 0.3 ^{NS}	2.0 ^{NS}	2.8 [*]	0.8 ^{NS}	- 1.2 ^{NS}	0.0	- 0.5 ^{NS}

* - significant at 5% probability level

** - significant at 1 % probability level

NS - non-significant

Table 3: Results of the joint regression analysis of diffident yield related traits for adequacy of data sets to additive-dominance model as obtained from 4 × 4 diallel cross.

Sr. no.	Characters	t – calculated value for regression coefficient b		Remarks	Conclusions
		b = 1	b = 0		
1	days to heading	0.10 ^{NS}	7.20 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
2	flag leaf area	1.11 ^{NS}	4.81 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
3	number of tillers per plant	0.41 ^{NS}	8.76 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
4	Plant height	-0.31 ^{NS}	10.4 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
5	Spike length	-0.44 ^{NS}	16.5 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
6	no. of spikelets per spike	0.22 ^{NS}	3.40 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
7	number of grains per spike	0.73 ^{NS}	5.70 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
8	grain weight per spike	0.19 ^{NS}	13.7 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
9	Seed index	0.41 ^{NS}	25.4 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis
10	Grain yield per plant	0.25 ^{NS}	14.2 ^{**}	Regression coefficient significantly different from zero but not from unity.	Data was fit for diallel analysis

* - significant at 0.05 % probability level

** - significant at 0.01 % probability level NS- non-significant

Graphical analysis (Figure 1. a – Figure 1. j) revealed that all yield related traits (under current study) of wheat were under the control of additive gene action with partial dominance as regression line cuts the Wr-axis above the origin and it passes from the parabola.

DISCUSSION

Development of early genotypes seems to be a priority to fit the wheat variety in intensive cropping systems and in this context, negative heterotic response for heading is desirable (Singh *et al.*, 2013). Our results reported highly significant negative heterosis which can be considered to produce transgressive segregates in later generations. These findings are strengthened with the findings of Singh *et al.*, 2007. who observed significant hybrid vigour for heading days in wheat germplasm. Flag leaf area has a critical role in proper grain development. Rashid *et al.* 2012 reported that about 75% of the photoassimilates that go into the seeds are produced by flag leaf. Heterosis for this trait seemed not

enough for exploitation. Similar type of results were reported by Singh *et al.*, (2013) who observed significant but low heterosis for flag leaf area in bread wheat which support these findings. Number of tillers directly contributes to grain yield. Positive heterosis for tillers per plant is therefore desirable in wheat (Kallimullah 2011). Comparative high value of heterosis for this traits was considered important to get transgressive segregants by selection in advanced generations. The findings are supported by Yagdi (2000) and Farooq *et al.*, (2005) who recorded significant hybrid vigour in number of tillers per plant.

Plant height is an important agronomic trait. Short stature wheat is preferred due to its better response to fertilizer and other inputs and therefore negative heterosis is desirable (Kallimullah 2011 - missing in the References). Negative heterosis for this trait can be fruitful in developing short stature varieties. The results are strengthened by the results of Akbar *et al.*, (2010) who also reported significant heterosis for this trait. Spike length is directly related to the

yield as long spikes contained more grains and it should be given due consideration during selection (Devi *et al.*, 2013 and Singh *et al.*, 2013). Thus, positive heterosis for spike length as in our study may be helpful in breeding programs. The results are supported by earlier findings of other researchers i.e. Yagdi (2000), Farooq *et al.*, (2005), Bilgin *et al.* (2011) and Singh *et al.* (2013) who reported similar results for this trait. Spikelets per spike is an effective yield component and a greater number would result in more grains per spike. Therefore, positive heterosis is desirable for this trait (Kashif and Khaliq 2004). The cross combination with high value of heterosis may be recommended for advanced generation selection to generate wheat genotypes with improved grain yield. These findings are in accordance with Chowdhry *et al.* (2001) who reported heterosis for spikelet number/spike. Number of grains per spike is an important agronomic character as it directly determines the yield potential of a genotype (Khan and Ali 2011). Highly significant better parent heterosis found in our study for this trait is supported by Yagdi (2000), Farooq *et al.* (2005), Singh *et al.*, (2007) and Devi *et al.* (2013) who investigated heterosis for number of grains/spike. Grain weight per spike is an important agronomic character contributing to yield, so increase in hybrid vigour is desirable for this trait (Bilgin *et al.*, 2011). The hybrid Renya-23 × Punjab-11 which expressed the highest possible degree of significant desired heterobeltiosis was identified as superior cross combination for getting transgressive segregants by making selection in advanced generations. Findings of Bilgin *et al.*, (2011) support our results who investigated heterosis for grain weight per spike. Seed index is an important yield related trait as significant variability in seed index / grain weight is essential for breeder to sort out genotypes with superior grain weight that result in higher grain yield (Hammad *et al.*, 2013). The hybrid combinations with high degree of heterobeltiosis for seed index can be used in future breeding programs to get superior genotypes by making selection in later generations. These findings are in agreement with Yagdi (2000), Chowdhry *et al.*, (2001), Akbar *et al.*, (2010), Bilgin *et al.*, (2011) and Devi *et al.*, (2013) who reported heterotic response of the crosses for seed index. Grain yield in crop improvement is ultimate objective of any breeding programme (Hammad *et al.*, 2013). High degree of heterosis for this trait is supported by Farooq *et al.*, (2005) and Akbar *et al.*, (2010) who reported heterotic effects for grain yield/plant.

Heredity control of yield and yield related traits plays an important role in any breeding program as success of selection in segregating generations depends on the knowledge of inheritance and heredity control of specific character. Hayman (1954) and Jinks (1954) graphical approach is considered as an authentic analysis to investigate the gene action controlling the heredity of different traits (Ul-Allah *et al.*, 2011). Graphical analysis revealed that all yield related traits (under current study) of wheat were under the control of additive gene action with partial dominance. These findings are in accordance with

other researchers (Ali *et al.*, 1999; *et al.*, 2005; Ul-Allah *et al.*, 2010; Ul-Allah *et al.*, 2011; Hammad *et al.*, 2013) who worked on genetics of wheat and reported similar results.

Conclusion: Although statistical significant better parent heterosis is present for all the traits but for none of the trait there is more than 20% heterosis. Presence of this low value of better parent heterosis suggest that heterosis breeding is not successful in wheat as it is a tough, time and labor consuming job with a small output. Rather than heterosis breeding we can use this heterosis in breeding program for selection of improved traits as selection seems fruitful for all the traits which are controlled by additive gene action with partial dominance.

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